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1652

#18  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/534,229C

DATE: 04/12/2002

TIME: 15:08:05

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\04122002\I534229C.raw

5 <110> APPLICANT: Kawakami, Akira  
6 Terami, Fumihiro  
9 <120> TITLE OF INVENTION: LOW TEMPERATURE EXPRESSION CHITINASE cDNAs AND METHOD FOR  
ISOLATING THE  
10 SAME  
13 <130> FILE REFERENCE: 107156-00004  
W--> 14 <140> CURRENT APPLICATION NUMBER: US 09/534,229C  
16 <141> CURRENT FILING DATE: 2000-03-24  
19 <160> NUMBER OF SEQ ID NOS: 8  
22 <170> SOFTWARE: PatentIn version 3.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 256  
27 <212> TYPE: PRT  
28 <213> ORGANISM: Triticum aestivum  
31 <400> SEQUENCE: 1  
33 Met Ala Arg Phe Ala Ala Leu Ala Val Cys Ala Ala Ala Leu Leu Leu  
34 1 5 10 15  
36 Ala Val Ala Ala Gly Gly Ala Ala Ala Gln Gly Val Gly Ser Val Ile  
37 20 25 30  
39 Thr Arg Ser Val Tyr Ala Ser Met Leu Pro Asn Arg Asp Asn Ser Leu  
40 35 40 45  
42 Cys Pro Ala Arg Gly Phe Tyr Thr Tyr Asp Ala Phe Ile Ala Ala Ala  
43 50 55 60  
45 Asn Thr Phe Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Asp Ile Lys  
46 65 70 75 80  
48 Arg Asp Leu Ala Ala Phe Phe Gly Gln Thr Ser His Glu Thr Thr Gly  
49 85 90 95  
51 Gly Thr Arg Gly Ala Ala Asp Gln Phe Gln Trp Gly Tyr Cys Phe Lys  
52 100 105 110  
54 Glu Glu Ile Ser Lys Ala Thr Ser Pro Pro Tyr Tyr Gly Arg Gly Pro  
55 115 120 125  
57 Ile Gln Leu Thr Gly Arg Ser Asn Tyr Asp Leu Ala Gly Arg Ala Ile  
58 130 135 140  
60 Gly Lys Asp Leu Val Ser Asn Pro Asp Leu Val Ser Thr Asp Ala Val  
61 145 150 155 160  
63 Val Ser Phe Arg Thr Ala Met Trp Phe Trp Met Thr Ala Gln Gly Asn  
64 165 170 175  
66 Lys Pro Ser Cys His Asn Val Ala Leu Arg Arg Trp Thr Pro Thr Ala  
67 180 185 190  
69 Ala Asp Thr Ala Ala Gly Arg Val Pro Gly Tyr Gly Val Ile Thr Asn  
70 195 200 205  
72 Ile Ile Asn Gly Gly Leu Glu Cys Gly Met Gly Arg Asn Asp Ala Asn  
73 210 215 220  
75 Val Asp Arg Ile Gly Tyr Tyr Thr Arg Tyr Cys Gly Met Leu Gly Thr

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76 225          230          235          240
78 Ala Thr Gly Gly Asn Leu Asp Cys Tyr Thr Gln Arg Asn Phe Ala Ser
79          245          250          255
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 323
83 <212> TYPE: PRT
84 <213> ORGANISM: Triticum aestivum
87 <400> SEQUENCE: 2
89 Met Ser Thr Leu Arg Ala Arg Cys Ala Thr Ala Val Leu Ala Val Val
90 1          5          10          15
92 Leu Ala Ala Ala Ala Val Thr Pro Ala Thr Ala Glu Gln Cys Gly Ser
93          20          25          30
95 Gln Ala Gly Gly Ala Lys Cys Ala Asp Cys Leu Cys Cys Ser Gln Phe
96          35          40          45
98 Gly Phe Cys Gly Thr Thr Ser Asp Tyr Cys Gly Pro Arg Cys Gln Ser
99          50          55          60
101 Gln Cys Thr Gly Cys Gly Gly Gly Gly Gly Val Ala Ser Ile Val
102 65          70          75          80
104 Ser Arg Asp Leu Phe Glu Arg Phe Leu Leu His Arg Asn Asp Ala Ala
105          85          90          95
107 Cys Leu Ala Arg Gly Phe Tyr Thr Tyr Asp Ala Phe Leu Ala Ala Ala
108          100          105          110
110 Gly Ala Phe Pro Ala Phe Gly Thr Thr Gly Asp Leu Asp Thr Arg Lys
111          115          120          125
113 Arg Glu Val Ala Ala Phe Phe Gly Gln Thr Ser His Glu Thr Thr Gly
114          130          135          140
116 Gly Trp Pro Thr Ala Pro Asp Gly Pro Phe Ser Trp Gly Tyr Cys Phe
117 145          150          155          160
119 Lys Gln Glu Gln Gly Ser Pro Pro Ser Tyr Cys Asp Gln Ser Ala Asp
120          165          170          175
122 Trp Pro Cys Ala Pro Gly Lys Gln Tyr Tyr Gly Arg Gly Pro Ile Gln
123          180          185          190
125 Leu Thr His Asn Tyr Asn Tyr Gly Pro Ala Gly Arg Ala Ile Gly Val
126          195          200          205
128 Asp Leu Leu Asn Asn Pro Asp Leu Val Ala Thr Asp Pro Thr Val Ala
129          210          215          220
131 Phe Lys Thr Ala Ile Trp Phe Trp Met Thr Thr Gln Ser Asn Lys Pro
132 225          230          235          240
134 Ser Cys His Asp Val Ile Thr Gly Leu Trp Thr Pro Thr Ala Arg Asp
135          245          250          255
137 Ser Ala Ala Gly Arg Val Pro Gly Tyr Gly Val Ile Thr Asn Val Ile
138          260          265          270
140 Asn Gly Gly Ile Glu Cys Gly Met Gly Gln Asn Asp Lys Val Ala Asp
141          275          280          285
143 Arg Ile Gly Phe Tyr Lys Arg Tyr Cys Asp Ile Phe Gly Ile Gly Tyr
144          290          295          300
146 Gly Asn Asn Leu Asp Cys Tyr Asn Gln Leu Ser Phe Asn Val Gly Leu
147 305          310          315          320
149 Ala Ala Gln

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Input Set : A:\PTO.VSK.txt

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152 <210> SEQ ID NO: 3
153 <211> LENGTH: 319
154 <212> TYPE: PRT
155 <213> ORGANISM: Triticum aestivum
158 <400> SEQUENCE: 3
160 Met Arg Gly Val Val Val Val Ala Met Leu Ala Ala Ala Phe Ala Val
161 1 5 10 15
163 Ser Ala His Ala Glu Gln Cys Gly Ser Gln Ala Gly Gly Ala Thr Cys
164 20 25 30
166 Pro Asn Cys Leu Cys Cys Ser Lys Phe Gly Phe Cys Gly Thr Thr Ser
167 35 40 45
169 Asp Tyr Cys Gly Thr Gly Cys Gln Ser Gln Cys Asn Gly Cys Ser Gly
170 50 55 60
172 Gly Thr Pro Val Pro Val Pro Thr Pro Ser Gly Gly Gly Val Ser Ser
173 65 70 75 80
175 Ile Ile Ser Gln Ser Leu Phe Asp Gln Met Leu Leu His Arg Asn Asp
176 85 90 95
178 Ala Ala Cys Leu Ala Lys Gly Phe Tyr Asn Tyr Gly Ala Phe Val Ala
179 100 105 110
181 Ala Ala Asn Ser Phe Ser Gly Phe Ala Thr Thr Gly Ser Thr Asp Val
182 115 120 125
184 Lys Lys Arg Glu Val Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr
185 130 135 140
187 Thr Gly Gly Trp Pro Thr Ala Pro Asp Gly Pro Tyr Ser Trp Gly Tyr
188 145 150 155 160
190 Cys Phe Asn Gln Glu Arg Gly Ala Thr Ser Asp Tyr Cys Thr Pro Ser
191 165 170 175
193 Ser Gln Trp Pro Cys Ala Pro Gly Lys Lys Tyr Phe Gly Arg Gly Pro
194 180 185 190
196 Ile Gln Ile Ser His Asn Tyr Asn Tyr Gly Pro Ala Gly Gln Ala Ile
197 195 200 205
199 Gly Thr Asp Leu Leu Asn Asn Pro Asp Leu Val Ala Ser Asp Ala Thr
200 210 215 220
202 Val Ser Phe Lys Thr Ala Leu Trp Phe Trp Met Thr Pro Gln Ser Pro
203 225 230 235 240
205 Lys Pro Ser Ser His Asp Val Ile Thr Gly Arg Trp Ser Pro Ser Gly
206 245 250 255
208 Ala Asp Gln Ala Ala Gly Arg Val Pro Gly Tyr Gly Val Ile Thr Asn
209 260 265 270
211 Ile Ile Asn Gly Gly Leu Glu Cys Gly Arg Gly Gln Asp Gly Arg Val
212 275 280 285
214 Ala Asp Arg Ile Gly Phe Tyr Lys Arg Tyr Cys Asp Leu Leu Gly Val
215 290 295 300
217 Ser Tyr Gly Asp Asn Leu Asp Cys Tyr Asn Gln Arg Pro Phe Ala
218 305 310 315

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220 &lt;210&gt; SEQ ID NO: 4

221 &lt;211&gt; LENGTH: 23

222 &lt;212&gt; TYPE: DNA

C--&gt; 223 &lt;213&gt; ORGANISM: Artificial

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\04122002\I534229C.raw

226 <220> FEATURE:  
 227 <221> NAME/KEY: misc\_feature  
 228 <222> LOCATION: (1)..(23)  
 229 <223> OTHER INFORMATION: Artificial primer.  
 232 <220> FEATURE:  
 233 <221> NAME/KEY: misc\_feature  
 234 <222> LOCATION: 12, 18  
 235 <223> OTHER INFORMATION: n can be one of a,c,t, or g  
 238 <400> SEQUENCE: 4  
 239 caccgagacca cngggcggtg ggc 23  
 242 <210> SEQ ID NO: 5  
 243 <211> LENGTH: 20  
 244 <212> TYPE: DNA  
 C--> 245 <213> ORGANISM: Artificial  
 249 <220> FEATURE:  
 250 <221> NAME/KEY: misc\_feature  
 251 <222> LOCATION: (1)..(20)  
 252 <223> OTHER INFORMATION: Artificial primer.  
 255 <220> FEATURE:  
 256 <221> NAME/KEY: misc\_feature  
 257 <222> LOCATION: 3  
 258 <223> OTHER INFORMATION: n can be one of a,c,t, or g  
 261 <400> SEQUENCE: 5  
 262 acnaatatca tcaacggcgg 20  
 265 <210> SEQ ID NO: 6  
 266 <211> LENGTH: 771  
 267 <212> TYPE: DNA  
 268 <213> ORGANISM: Triticum aestivum  
 271 <220> FEATURE:  
 272 <221> NAME/KEY: misc\_feature  
 273 <222> LOCATION: (1)..(771)  
 274 <223> OTHER INFORMATION: cDNA  
 277 <400> SEQUENCE: 6  
 278 atggcgaggt ttgctgccct cgccgtgtgc gccgccgcgc tctgtctgc cgtggcgggc 60  
 280 ggggggtgccg cggcgagggg cgtggggtcg gtcacacgc ggtcggtgta cgcgagcact 120  
 282 ctgcccacc gcgacaactc gctgtgcccg gccagagggg tctacacgta cgacgccttc 180  
 284 atcgccgccg ccaacacctt cccgggcttc gccaccaccg gcagcgccga cgacatcaag 240  
 286 cgcgacctcg ccgccttctt cggccagacc tcccacgaga ccaccggagg gacgagaggc 300  
 288 gctgccgacc agttccagtg gggctactgc ttcaaggaa agataagcaa ggccacgtcc 360  
 290 ccaccatact atggacgggg acccatccaa ttgacagggc ggtccaacta cgatcttgcc 420  
 292 gggagagcga tcgggaagga cctgggtgagc aaccacgacc tagtgtccac ggacgcggtg 480  
 294 gtgtccttca ggacggccat gtggttctgg atgacggcgc agggaaacaa gccgtcgtgc 540  
 296 cacaacgtcg ccctacgccg ctggacgccg acggccgccg acaccgctgc cggcagggta 600  
 298 cccggatacg gagtgatcac caatatcatc aacggcgggc tcgagtgcgg aatggggcgg 660  
 300 aacgacgcca acgtcgaccg catcggttac tacacgcgct actgcggcat gctcggcacg 720  
 302 gccaccggag gcaacctcga ctgctacacc cagaggaact tcgctagcta g 771  
 305 <210> SEQ ID NO: 7  
 306 <211> LENGTH: 972  
 307 <212> TYPE: DNA

## RAW SEQUENCE LISTING

DATE: 04/12/2002

PATENT APPLICATION: US/09/534,229C

TIME: 15:08:05

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\04122002\I534229C.raw

308 <213> ORGANISM: *Triticum aestivum*

311 &lt;220&gt; FEATURE:

312 &lt;221&gt; NAME/KEY: misc\_feature

313 &lt;222&gt; LOCATION: (1)..(972)

314 &lt;223&gt; OTHER INFORMATION: cDNA

317 &lt;400&gt; SEQUENCE: 7

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318 atgtccacgc tgagagcgcg gtgtgcgacg gccgtcctgg ccgtcgtcct ggcgggcgcc      60
320 gcggtcacgc cggccacggc cgagcagtg cgcctcgcaag ccggcggcgc caagtgcgcc      120
322 gactgcctgt gctgcagcca gtctgggttc tgcggcacca cctccgacta ctgcggcccc      180
324 cgctgccaga gccagtgcac tggctgcggt ggcgggcgcg gcgggggtggc ctccatcgtg      240
326 tccagggacc tcttcgagcg gtctctgctc catcgcaacg acgcagcgtg cctggccccgc      300
328 gggttctaca cgtacgacgc cttcttgccc gccgcggcg cgttcccggc cttcggcacc      360
330 accggagacc tggacacgcg gaagcgggag gtggcgccct tcttcggcca gacctctcac      420
332 gagaccaccg gcgggtggcc caccgcgcc gccgcccct tctcatgggg ctactgcttc      480
334 aagcaggagc agggctcgcc gccgagctac tgcgaccaga gcgcgactg gccgtgcgca      540
336 ccgggcaagc agtactatgg ccgcggcccc atccagctca cccacaacta caactacgga      600
338 ccggcggggc gcgcaatcgg ggtggacctg ctgaacaatc cggacctggt ggccacggac      660
340 ccgacagtgg cgttcaagac ggcgatatgg ttctggatga cgacgcagtc caacaagccg      720
342 tcgtgccatg acgtgatcac ggggctgtgg actccgacgg ccagggatag cgagccggga      780
344 cgggtacccg ggtatggtgt catcaccaac gtcataacg gcgggatcca atgcggcatg      840
346 gggcagaacg acaaggtggc ggatcggatc gggttctaca agcgtattg tgacattttc      900
348 ggcacggct acgggaataa cctcgactgc tacaaccaat tgcgttcaa cgttgggctc      960
350 gcggcacagt ga                                         972

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353 &lt;210&gt; SEQ ID NO: 8

354 &lt;211&gt; LENGTH: 960

355 &lt;212&gt; TYPE: DNA

356 <213> ORGANISM: *Triticum aestivum*

360 &lt;220&gt; FEATURE:

361 &lt;221&gt; NAME/KEY: misc\_feature

362 &lt;222&gt; LOCATION: (1)..(960)

363 &lt;223&gt; OTHER INFORMATION: cDNA

366 &lt;400&gt; SEQUENCE: 8

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367 atgagaggag ttgtggtggt ggccatgctg gccgcggcct tcgccgtgtc tgcgcacgcc      60
369 gagcaatgcg gctcgcaggc cggcggggcg acgtgcccc aactgcctctg ctgcagcaag      120
371 ttcggtttct gcggcaccac ctccgactac tgcggcaccg gctgccagag ccagtgcagt      180
373 ggctgcagcg gcggcaccac ggtaccggta ccgaccccc cggcgggcg cgctctcctcc      240
375 attatctcgc agtcgtctt cgaccagatg ctgctgcacc gcaacgcagc ggctgcctg      300
377 gccaaagggt tctacaacta cggcgccctt gtcgcggcg ccaactcgtt ctcgggcttc      360
379 gcgaccacag gtagcaccga cgtcaagaag cgcgaggtgg ccgcgttct cgtcagact      420
381 tcccacgaga cgaccggcgg gtggccgacg gcgcccgcg gccctactc ctggggctac      480
383 tgcctcaacc aggagcgcgg cgccacctcc gactactgca cgcgagctc gcagtggcca      540
385 tgtgcgcgg gcaagaagta cttcggggcg gggcccatcc agatctcaca caactacaac      600
387 tacggggcgg cggggcaggc catcggcacc gacctgctca acaaccggga ccttgtggcg      660
389 tcggagcgca ccgtgtcgtt taagacggcg ttgtggttct ggatgacgcc gcaatcaccc      720
391 aagccttcga gccacgacgt gatcacgggc cgggtggagc cctcggggcg cgaccaggcg      780
393 gcggggaggg tgcttgggta cgggtgtgat accaacaatc tcaacggtgg gctcagatgc      840
395 gggcgcgggc aggacggcgg tgcgcggac cggtatcggg tctacaagcg ctactgcgac      900
397 ctcttggcg tcagctacg tgacaacctg gactgtctca accaaaggcc gttcgcatag      960

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/534,229C

DATE: 04/12/2002  
TIME: 15:08:06

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF3\04122002\I534229C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 12,18  
Seq#:5; N Pos. 3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/534,229B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.